



# Example: Comparison of proteins of sequenced microbial genomes

- 570 microbial genomes sequenced (Jul. 07)
- 5 millions proteins
- Microbiogenomics project
  - Optimal extraction of relevant information from complex and heterogeneous data provided by exhaustive genomic comparisons
  - IGM+LRI/Univ. Paris-Sud, MIG/INRA
- Protein-Protein Network
  - Compute evolution distance
  - Cut above threshold (250 PAM units)
  - Cluster
  - Cut weak links (try to)
- Visualize!











## Comparing the readability of the 2 representations

- The Tasks:
- Tasks related to the overview – Number of vertices
  - Number of arcs
- Tasks related to graph elements
  - Finding an element (a vertex, a link)
     Finding the most connected vertex (a)
  - Finding the most connected vertex (a central actor, a pivot, a hub)
     Finding a common neighbor
  - Finding a path
- Random graphs (3 sizes et 3 densities)
- 2 representations: Node-Link + Matrix
  Results:
- Node-link diagrams are preferable for small sparse graphs (20 vertices)
- Matrices are more readable wrt dense graphs and medium/large graphs ( > 20 vertices) wrt the selected tasks, except paths

#### References:

Mohammad Ghoniem, Jean-Daniel Fekete and Philippe Castagliola Readability of Graphs Using Node-Link and Matrix-Based Representations: Controlled Experiment and Statistical Analysis, Information Visualization Journal, 4(2), Palgrave Macmillan, Summer 2005, pp. 114-135.



representations (Node-Link in blue, Matrix in red)





















































Results				
Dataset	Vertices	Edges	Load (sec)	Reorder (sec)
InfoVis04	1,000	1,000	10	10
Protein- Protein	30,000	1,000,000	20	20
Wikipedia FR	500,000	6,000,000	65	70

### Conclusion

- Matrix representation is a powerful complement to NL
- Good for
  - Dense networks
  - Filtering and selection
- Once filtered and reduced, the network can be visualized with a NL
- Hybrid representations
  - improve understanding of matrices
  - combine the best of both worlds



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